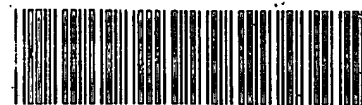


217 #10



OIPE

RAW SEQUENCE LISTING

DATE: 02/14/2002

PATENT APPLICATION: US/09/758,017A

TIME: 10:10:39

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3 <110> APPLICANT: Lanes, Olav
4      Willasen, Nils Peder
5      Guddal, Per Henrik
6      Gjellesvik, Dag Rune
8 <120> TITLE OF INVENTION: Cod uracil-DNA glycosylase, gene coding therefore,
9      recombinant DNA containing said gene or operative parts
10     thereof, a method for preparing said protein and the
11     use of said protein or said operative pa
13 <130> FILE REFERENCE: U013209-3
15 <140> CURRENT APPLICATION NUMBER: 09/758,017A
16 <141> CURRENT FILING DATE: 2001-01-10
18 <150> PRIOR APPLICATION NUMBER: 2000 5428
19 <151> PRIOR FILING DATE: 2000-10-27
21 <150> PRIOR APPLICATION NUMBER: 2000 0163
22 <151> PRIOR FILING DATE: 2000-01-12
24 <160> NUMBER OF SEQ ID NOS: 19
26 <170> SOFTWARE: PatentIn Ver. 2.0
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29 <211> LENGTH: 1283
30 <212> TYPE: DNA
31 <213> ORGANISM: Gadus morhua
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (18)..(920)
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39           Met Leu Phe Lys Leu Gly Leu Cys Gln Arg Cys
40           1             5             10
42 ata tca tca aat cgg gtg tta cca ggt tta cta att ccc caa act tta      98
43 Ile Ser Ser Asn Arg Val Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu
44           15             20             25
46 tgt ttt tct aaa tta atg aag ata acg ccg aag aaa ctg agg tcc tca      146
47 Cys Phe Ser Lys Leu Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser
48           30             35             40
50 aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg gag cag ctg      194
51 Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu
52           45             50             55
54 gaa aga atg gcc aaa aat aag aaa gca gcg ctt gac aag att aga gca      242
55 Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala
56           60             65             70             75
58 aaa gca acg cct gca ggt ttc gga gag act tgg aga aga gag ctg gct      290
59 Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala
60           80             85             90

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62 gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc ttt gta gct 338
63 Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala
64          95          100          105
66 gat gag agg agc cgt cac acc gtc tac cca ccg gct gat caa gtg tac 386
67 Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr
68          110          115          120
70 agt tcg aca gag atg tgt gac att caa gat gtg aaa gta gtg att cta 434
71 Ser Ser Thr Glu Met Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu
72          125          130          135
74 ggc cag gac cct tac cac ggt ccc aac caa gca cat gga ctc tgt ttc 482
75 Gly Gln Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly Leu Cys Phe
76          140          145          150          155
78 agt gtg caa aag cca gtt ccc cct ccc ccc agt ctc gtg aac ata tac 530
79 Ser Val Gln Lys Pro Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr
80          160          165          170
82 aaa gaa ttg tgt acc gac att gat ggc ttc aag cat cct gga cat gga 578
83 Lys Glu Leu Cys Thr Asp Ile Asp Gly Phe Lys His Pro Gly His Gly
84          175          180          185
86 gat cta agc gga tgg gca aaa caa ggg gtg ctg ctg ctt aac gcg gtg 626
87 Asp Leu Ser Gly Trp Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val
88          190          195          200
90 ctg acc gtg cgg gcc cat cag gcc aac tcc cac aag gac aga ggc tgg 674
91 Leu Thr Val Arg Ala His Gln Ala Asn Ser His Lys Asp Arg Gly Trp
92          205          210          215
94 gag acc ttc acc gac gct gtg atc aag tgg ctg agc gtc aac cgg gaa 722
95 Glu Thr Phe Thr Asp Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu
96          220          225          230          235
98 gga gtc gtt ttc ctg ttg tgg ggc tca tac gcc cat aag aag gga gcg 770
99 Gly Val Val Phe Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala
100          240          245          250
102 acc atc gac agg aaa cgt cac cat gtc ttg caa gct gtt cat cca tct 818
103 Thr Ile Asp Arg Lys Arg His His Val Leu Gln Ala Val His Pro Ser
104          255          260          265
106 cct ttg tct gct cat cgt ggg ttc ctt ggt tgt aag cac ttc tcc aag 866
107 Pro Leu Ser Ala His Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys
108          270          275          280
110 gct aac ggg ctg ctg aaa cta tct ggg acg gag cct ata aac tgg aga 914
111 Ala Asn Gly Leu Leu Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg
112          285          290          295
114 gca ctc taactcttta tgctgcctta tactgttaac tgttttaaga tgaacatcac 970
115 Ala Leu
116 300
118 actatatattt ctacagcttt tccaagttca aaccaatcta taagctttca tttgtctttt 1030
120 ggaatgatgc tgcttttggg cggtttttaga tacttaaaac actttaccac tctgccatgt 1090
122 tgactcatgt tcagtcataa taactttcac aacttgaaca aaaatgttat tttataattg 1150
124 attatattct gtacattaaa gattgttttt tcccaggct gtttcatagg tactaggata 1210
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Output Set: N:\CRF3\02142002\I758017A.raw

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132 <211> LENGTH: 301
133 <212> TYPE: PRT
134 <213> ORGANISM: Gadus morhua
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140 Val Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu Cys Phe Ser Lys Leu
141           20           25           30
143 Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
144           35           40           45
146 Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
147           50           55           60
149 Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
150   65           70           75           80
152 Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
153           85           90           95
155 Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
156           100          105          110
158 His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Ser Thr Glu Met
159           115          120          125
161 Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
162           130          135          140
164 His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
165   145          150          155          160
167 Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr
168           165          170          175
170 Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp
171           180          185          190
173 Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val Leu Thr Val Arg Ala
174           195          200          205
176 His Gln Ala Asn Ser His Lys Asp Arg Gly Trp Glu Thr Phe Thr Asp
177           210          215          220
179 Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu Gly Val Val Phe Leu
180   225          230          235          240
182 Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys
183           245          250          255
185 Arg His His Val Leu Gln Ala Val His Pro Ser Pro Leu Ser Ala His
186           260          265          270
188 Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys Ala Asn Gly Leu Leu
189           275          280          285
191 Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg Ala Leu
192           290          295          300
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196 <211> LENGTH: 1355
197 <212> TYPE: DNA
198 <213> ORGANISM: Gadus morhua
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (90)..(992)

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204 <400> SEQUENCE: 3

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208                               Met Ile Gly Gln Gln His Ile Asn
209                               1                               5
211 tct ttc ttc tca cca gtt tca aaa aag aga gtt tca aag gaa tta ggt 161
212 Ser Phe Phe Ser Pro Val Ser Lys Lys Arg Val Ser Lys Glu Leu Gly
213 10 15 20
215 aaa acc gaa aag cat gcc gaa gaa gtt cag ata acg ccg aag aaa ctg 209
216 Lys Thr Glu Lys His Ala Glu Glu Val Gln Ile Thr Pro Lys Lys Leu
217 25 30 35 40
219 agg tcc tca aat gtg gaa caa aag acg tca tgc cca cag ctt tca gtg 257
220 Arg Ser Ser Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val
221 45 50 55
223 gag cag ctg gaa aga atg gcc aaa aat aag aaa gca gcg ctt gac aag 305
224 Glu Gln Leu Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys
225 60 65 70
227 att aga gca aaa gca acg cct gca ggt ttc gga gag act tgg aga aga 353
228 Ile Arg Ala Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg
229 75 80 85
231 gag ctg gct gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc 401
232 Glu Leu Ala Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser
233 90 95 100
235 ttt gta gct gat gag agg agc cgt cac acc gtc tac cca ccg gct gat 449
236 Phe Val Ala Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp
237 105 110 115 120
239 caa gtg tac agt tgg aca gag atg tgt gac att caa gat gtg aaa gta 497
240 Gln Val Tyr Ser Trp Thr Glu Met Cys Asp Ile Gln Asp Val Lys Val
241 125 130 135
243 gtg att cta ggc cag gac cct tac cac ggt ccc aac caa gca cat gga 545
244 Val Ile Leu Gly Gln Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly
245 140 145 150
247 ctc tgt ttc agt gtg caa aag cca gtt ccc cct ccc ccc agt ctc gtg 593
248 Leu Cys Phe Ser Val Gln Lys Pro Val Pro Pro Pro Pro Ser Leu Val
249 155 160 165
251 aac ata tac aaa gaa ttg tgt acc gac att gat ggc ttc aag cat cct 641
252 Asn Ile Tyr Lys Glu Leu Cys Thr Asp Ile Asp Gly Phe Lys His Pro
253 170 175 180
255 gga cat gga gat cta agc gga tgg gca aac aag ggg tgc tgc tgc tta 689
256 Gly His Gly Asp Leu Ser Gly Trp Ala Asn Lys Gly Cys Cys Cys Leu
257 185 190 195 200
259 acg cgc tgc ctg acc gtg cgg gcc cat cag gcc aac tcc cac aag gac 737
260 Thr Arg Cys Leu Thr Val Arg Ala His Gln Ala Asn Ser His Lys Asp
261 205 210 215
263 aga ggc tgg gag acc tcc acc gac gct gtg atc aag tgg ctg agc gtc 785
264 Arg Gly Trp Glu Thr Ser Thr Asp Ala Val Ile Lys Trp Leu Ser Val
265 220 225 230
267 aac cgg gaa gga gtg gtt ttc ctg ttc tgg ggc tca tac gcc cat aag 833
268 Asn Arg Glu Gly Val Val Phe Leu Phe Trp Gly Ser Tyr Ala His Lys

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269          235          240          245
271 aag gga gcg acc atc gac agg aaa cgt cac cat gtc ttg caa gct ctt      881
272 Lys Gly Ala Thr Ile Asp Arg Lys Arg His His Val Leu Gln Ala Leu
273          250          255          260
275 cat cca tct cct ttg tct gct cat cgt ggg ttc ctt ggt tgt aag cac      929
276 His Pro Ser Pro Leu Ser Ala His Arg Gly Phe Leu Gly Cys Lys His
277 265          270          275          280
279 ttc tcc aag gct aac ggg ctg ctg aaa cta tct ggg acg gag cct ata      977
280 Phe Ser Lys Ala Asn Gly Leu Leu Lys Leu Ser Gly Thr Glu Pro Ile
281          285          290          295
283 aac tgg aga gca ctc taactcttta tgctgcctta tactgttaac tgttttaaga      1032
284 Asn Trp Arg Ala Leu
285          300
287 tgaacatcac actatatctt ctacagcttt tccaagttca aaccaatcta taagctttca      1092
289 tttgtctttt ggaatgatgc tgcttttggt cggttttaga tacttaaaac actttaccac      1152
291 tctgccatgt tgactcatgt tcagtcaata taactttcac aacttgaaca aaaatggtat      1212
293 tttataattg attatatctt gtacattaaa gattgttttt ttcccaggct gtttcatagg      1272
295 tactaggata ttaaactggt attaacctat tttccatgat gtcaactgct taagttttta      1332
297 tgcagaaata aattatatat tta
298                                     1355
300 <210> SEQ ID NO: 4
301 <211> LENGTH: 301
302 <212> TYPE: PRT
303 <213> ORGANISM: Gadus morhua
305 <400> SEQUENCE: 4
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309 Lys Arg Val Ser Lys Glu Leu Gly Lys Thr Glu Lys His Ala Glu Glu
310          20          25          30
312 Val Gln Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
313          35          40          45
315 Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
316          50          55          60
318 Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
319 65          70          75          80
321 Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
322          85          90          95
324 Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
325          100          105          110
327 His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Trp Thr Glu Met
328          115          120          125
330 Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
331          130          135          140
333 His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
334 145          150          155          160
336 Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr
337          165          170          175
339 Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp
340          180          185          190
342 Ala Asn Lys Gly Cys Cys Cys Leu Thr Arg Cys Leu Thr Val Arg Ala

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VERIFICATION SUMMARY

DATE: 02/14/2002

PATENT APPLICATION: US/09/758,017A

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